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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/302,863

DATE: 09/03/1999  
TIME: 10:56:44

Input Set: I302863.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

# ENTERED

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1  <110> APPLICANT: Goodwin, Raymond G
2      Din, Wanwan S.
3  <120> TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
4  <130> FILE REFERENCE: 2519
5  <140> CURRENT APPLICATION NUMBER: US/09/302,863
6  <141> CURRENT FILING DATE: 1999-04-30
7  <160> NUMBER OF SEQ ID NOS: 5
8  <170> SOFTWARE: PatentIn Ver. 2.0
9  <210> SEQ ID NO 1
10 <211> LENGTH: 1377
11 <212> TYPE: DNA
12 <213> ORGANISM: Human
13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (14)..(892)
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18              Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
19              1              5              10
20      agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg      97
21      Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
22              15              20              25
23      gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg      145
24      Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
25              30              35              40
26      ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc      193
27      Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
28              45              50              55              60
29      acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc      241
30      Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
31              65              70              75
32      aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc      289
33      Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
34              80              85              90
35      tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc      337
36      Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
37              95              100              105
38      agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga      385
39      Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
40              110              115              120
41      gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag      433
42      Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu
43              125              130              135              140
44      cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt      481

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45      His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser
46                      145                      150                      155
47      gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt      529
48      Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys
49                      160                      165                      170
50      gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag      577
51      Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys
52                      175                      180                      185
53      agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt      625
54      Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser
55                      190                      195                      200
56      ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg      673
57      Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val
58      205                      210                      215                      220
59      agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag      721
60      Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu
61                      225                      230                      235
62      tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac      769
63      Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp
64                      240                      245                      250
65      ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg      817
66      Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
67                      255                      260                      265
68      cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg      865
69      Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val
70                      270                      275                      280
71      cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggaggagg      912
72      Pro Ala Gln Glu Gly Gly Pro Gly Ala
73      285                      290
74      aaaggaggag ggagagagat ggagaggagg ggagagagaa agagagggtg ggagagggga 972
75      gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032
76      gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092
77      ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152
78      gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggagggtc 1212
79      ggggcactct gagtcccagt tcccagtgcg gctgtaggtc gtcacacact aaccacacgt 1272
80      gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctcctc ctggagaata 1332
81      aaaccttttg cagctgcctt tcctcaaaaa aaaaaaaaaa aaaaaa      1377
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84      <212> TYPE: PRT
85      <213> ORGANISM: Human
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88          1              5              10              15
89      Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
90          20              25              30
91      Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
92          35              40              45
93      Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
94          50              55              60

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95 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
 96 65 70 75 80  
 97 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
 98 85 90 95  
 99 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
 100 100 105 110  
 101 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
 102 115 120 125  
 103 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
 104 130 135 140  
 105 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
 106 145 150 155 160  
 107 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
 108 165 170 175  
 109 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
 110 180 185 190  
 111 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
 112 195 200 205  
 113 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
 114 210 215 220  
 115 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
 116 225 230 235 240  
 117 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
 118 245 250 255  
 119 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
 120 260 265 270  
 121 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu  
 122 275 280 285  
 123 Gly Gly Pro Gly Ala  
 124 290

125 &lt;210&gt; SEQ ID NO 3

126 &lt;211&gt; LENGTH: 1057

127 &lt;212&gt; TYPE: DNA

128 &lt;213&gt; ORGANISM: Human

129 &lt;220&gt; FEATURE:

130 &lt;221&gt; NAME/KEY: CDS

131 &lt;222&gt; LOCATION: (58)..(912)

132 &lt;400&gt; SEQUENCE: 3

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 134 atg gat gac tcc aca gaa agg gag cag tca cgc ctt act tct tgc ctt 105  
 135 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu  
 136 1 5 10 15  
 137 aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 153  
 138 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro  
 139 20 25 30  
 140 cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 201  
 141 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu  
 142 35 40 45  
 143 gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 249  
 144 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val

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145	50	55	60	
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147	Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg			
148	65 70 75 80			
149	gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga	345		
150	Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly			
151	85 90 95			
152	gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg	393		
153	Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu			
154	100 105 110			
155	aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac	441		
156	Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn			
157	115 120 125			
158	agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa	489		
159	Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln			
160	130 135 140			
161	gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa	537		
162	Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys			
163	145 150 155 160			
164	gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt	585		
165	Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser			
166	165 170 175			
167	gcc cta gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac	633		
168	Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr			
169	180 185 190			
170	ttt ttt ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg	681		
171	Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met			
172	195 200 205			
173	gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg	729		
174	Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu			
175	210 215 220			
176	agt ctg gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta	777		
177	Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu			
178	225 230 235 240			
179	ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga	825		
180	Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly			
181	245 250 255			
182	gat gaa ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg	873		
183	Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu			
184	260 265 270			
185	gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt	922		
186	Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu			
187	275 280 285			
188	acaccatgtc tgtagctatt ttcctccctt tctctgtacc tctaagaaga aagaatctaa	982		
189	ctgaaaatac caaaaaaaaaa aaaaaaaaaa aaagatcttt aattaagcgg ccgcaagctt	1042		
190	attcccttta gtgag	1057		

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192 &lt;211&gt; LENGTH: 285

193 &lt;212&gt; TYPE: PRT

194 &lt;213&gt; ORGANISM: Human

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198 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
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200 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
201 35 40 45
202 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
203 50 55 60
204 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
205 65 70 75 80
206 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
207 85 90 95
208 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
209 100 105 110
210 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
211 115 120 125
212 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
213 130 135 140
214 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
215 145 150 155 160
216 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
217 165 170 175
218 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
219 180 185 190
220 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
221 195 200 205
222 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
223 210 215 220
224 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225 225 230 235 240
226 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
227 245 250 255
228 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
229 260 265 270
230 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
231 275 280 285
232 <210> SEQ ID NO 5
233 <211> LENGTH: 232
234 <212> TYPE: PRT
235 <213> ORGANISM: human
236 <400> SEQUENCE: 5
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239 Val Ala Leu Ala Ala Pro Ser Lys Ser Lys Arg Arg Thr Ser Ser Asp
240 20 25 30
241 Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
242 35 40 45
243 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
244 50 55 60

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VERIFICATION SUMMARY  
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